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Research Article

Three new species of *Favolaschia* (Mycenaceae, Agaricales) from South China

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Abstract

The genus *Favolaschia* within the family Mycenaceae is characterised by the gelatinous basidiomata with poroid hymenophore and most species inhabit monocotyledonous plants. In this study, many samples covering a wide geographic range in China were examined morphologically and phylogenetically using concatenated ITS1-5.8S-ITS2-nLSU sequence data. Three new species clustering in *Favolaschia* sect. *Anechinus*, namely *Favolaschia imbricata*, *F. miscanthi* and *F. sinarundinariae*, are described. *Favolaschia imbricata* is characterised by imbricate basidiomata with pale grey to greyish colour when fresh and broadly ellipsoid basidiospores measuring 7–9 × 5–6.8 µm; *F. miscanthi* is characterised by satin white basidiomata when fresh, broadly ellipsoid basidiospores measuring 7.5–10 × 5.5–7 µm and inhabit rotten *Miscanthus*; *F. sinarundinariae* is characterised by greyish-white basidiomata when fresh, dark grey near the base upon drying, broadly ellipsoid to subglobose basidiospores measuring 7–9 × 5–7 µm and inhabit dead *Sinarundinaria*. The differences amongst the new species and their morphologically similar and phylogenetically related species are discussed. In addition, an updated key to 19 species of *Favolaschia* found in China is provided.

Key words: New taxa, phylogeny, taxonomy, wood-decaying fungi

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Introduction

The genus *Favolaschia* (Pat.) Pat., typified by *F. gaillardia* (Pat.) Pat. (Patouillard 1887), belongs to the Mycenaceae Overeem (Agaricales) (Moncalvo et al. 2002; Bodensteiner et al. 2004). It is characterised by gelatinous basidiomata with poroid hymenophore, a monomitic hyphal system, a gelatinous hyphal structure, the presence of gloeocystidia and acanthocystida which are terminal, mostly swollen tips of hyphae covered by outgrowths (Clémençon 1977) and amyloid basidiospores (Singer 1945, 1974; Gillen et al. 2012; Capelari et al. 2013; Magnago et al. 2013; Zhang and Dai 2021; Zhang et al. 2023). *Favolaschia* species have a worldwide distribution and prefer humid climates with the highest species diversity in subtropical to tropical zones (Singer 1974; Gillen et al.

2012; Magnago et al. 2013). The basidiomata are found mostly on decaying parts of monocotyledonous plants, as well as ferns and cause white rot (Singer 1974; Gillen et al. 2012).

A total of 119 records of *Favolaschia* are listed in Index Fungorum (http://www.indexfungorum.org) and around 60 species are accepted (Johnston et al. 2006; Gillen et al. 2012; Magnago et al. 2013). The name "*Favolaschia*" was first introduced by Patouillard (1887) as a section of *Laschia* Fr and treated at a generic level later (Patouillard and Lagerheim 1892). The taxonomic history of the genus has been systematically compiled by Singer (1974) and Johnston et al. (2006). Singer (1974) divided *Favolaschia* into two sections, based on morphological studies, namely section *Favolaschia* Singer and section *Anechinus* Singer. Amongst them, taxa of *F.* sect. *Favolaschia* is characterised by having mostly orange, yellow, red, lateritious or pink pileus and the presence of acanthocytes in pileipellis. Inversely, taxa of *F.* sect. *Anechinus* are characterised by lacking acanthocystidia or replaced by diverticulate hyphae. Later, Johnston et al. (2006), Gillen et al. (2012) and Magnago et al. (2013) confirmed the two sections by phylogenetic analyses.

Recently, the systematic study of *Favolaschia* in China has gradually increased. Tolgor et al. (2021) investigated the phylogenetic relationships of *Favolaschia* and its related genera in Mycenaceae and reported four species distributed in China. Zhang and Dai (2021) investigated phylogenetic analysis of the genus *Favolaschia*, based on a large sample and revealed four new species in the *F. calocera* complex. Until Zhang et al. (2023) re-summarised the species diversity, phylogenetic relationships, divergence time and potential geographic distribution using a large number of samples covering a wide geographic range in China. To date, 16 species of *Favolaschia* have been reported from China, based on phylogenetic analyses, namely, *F. brevibasidiata* Q.Y. Zhang and Y.C. Dai, *F. brevistipitata* Q.Y. Zhang and Y.C. Dai, *F. longistipitata* Q.Y. Zhang and Y.C. Dai, *F. minutissima* Q.Y. Zhang and Y.C. Dai, *F. bannaensis* Q.Y. Zhang & Y.C. Dai, *F. crassipora* Q.Y. Zhang & Y.C. Dai, *F. flabelliformis* Q.Y. Zhang & Y.C. Dai, *F. manipularis* (Berk.) Teng, *F. peziziformis* (Berk. and M.A. Curtis) Kuntze, *F. pustulosa* (Jungh.) Kuntze, *F. rigida* Q.Y. Zhang & Y.C. Dai, *F. semicircularis* Q.Y. Zhang & Y.C. Dai, *F. subpustulosa* Q.Y. Zhang & Y.C. Dai, *F. tenuissima* Q.Y. Zhang & Y.C. Dai, *F. tephroleuca* Q.Y. Zhang & Y.C. Dai and *F. tonkinensis* (Pat.) Kuntze; the first four species belong to the *F. calocera* complex of the *F.* sect. *Favolaschia*; while the others belong to the *F.* sect. *Anechinus* (Zhang and Dai 2021; Guo et al. 2022; Ma et al. 2022; Wu et al. 2022a; Dong et al. 2023; Zhang et al. 2023).

During a study on wood-rotting fungi from south China, several samples belonging to *Favolaschia* were collected and three unknown species were morphologically distinguished. To confirm the affinity of the taxa, phylogenetic analysis was performed, based on a combined sequence dataset of ITS1-5.8S-ITS2-nLSU.

Materials and methods

Morphological studies

The specimens were collected from Guangxi Autonomous Region, Guangdong and Sichuan Provinces in south China and the specific locations were marked in Fig. 1. They were deposited in the Fungarium of the Institute of Microbiology, Beijing Forestry University (BJFC), Beijing, China. Macro-morphological descrip-

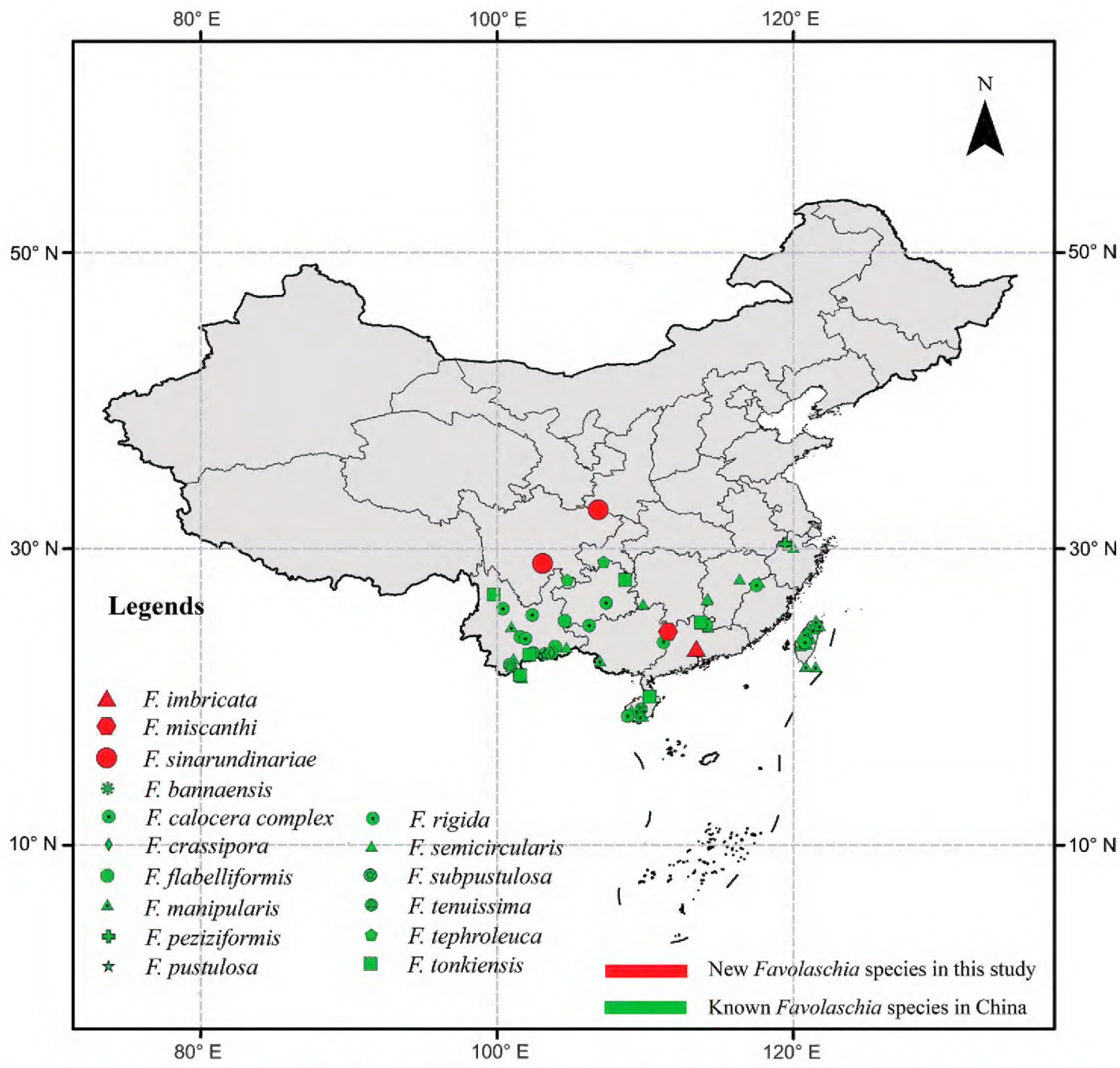

Figure 1. The geographical locations of *Favolaschia* species distributed in China (the base map of China was obtained from the Map Technology Review Center, Department of Natural Resources, http://bzdt.ch.mnr.gov.cn/).

tions were based on field notes and dried specimens. Microscopic features were examined and described in 5% KOH (potassium hydroxide) and 2% phloxine B ($C_{20}H_2Br_4Cl_4Na_2O_5$) with a magnification of up to 1,000× using a Nikon Eclipse 80i microscope and phase contrast illumination. Colour terms followed Kornerup and Wanscher (1978) and Petersen (1996). A Nikon Digital Sight DS-L3 camera was used to photograph microscopic structures. Other reagents, including Cotton Blue and Melzer's reagents were used to observe the micromorphology structures following Zhang et al. (2023). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. Thirty basidiospores from each specimen were measured. The following abbreviations are used: IKI = Melzer's reagent, IKI+ = amyloid; CB = Cotton Blue, CB– = acyanophilous in Cotton Blue; L = arithmetic average of basidiospores length, W = arithmetic average of basidiospores width, Q = L/W ratios, (*n* = x/y) = the number of spores (x) measured from a given number of specimens (y).

DNA extraction and sequencing

A cetyl trimethylammonium bromide (CTAB) rapid plant genome extraction kit (Aidlab Biotechnologies, Co., Ltd., Beijing, China) was used to extract DNA (Wu et al. 2020, 2022b). The ITS1-5.8S-ITS2 region was amplified with the primer pair ITS5/ITS4 (White et al. 1990) using the following protocol: initial denaturation at 95 °C for 4 min, followed by 34 cycles at 94 °C for 40 s, 54 °C for 45 s

and 72 °C for 1 min and final extension at 72 °C for 10 min. The nLSU region was amplified with the primer pair LR0R/LR7 (White et al. 1990) using the following protocol: initial denaturation at 94 °C for 1 min, followed by 34 cycles at 94 °C for 30 s, 50 °C for 1 min and 72 °C for 1.5 min and final extension at 72 °C for 10 min. The PCR products were purified and sequenced by the Beijing Genomics Institute (BGI), China with the same primers. The newly-generated sequences in this study have been deposited in GenBank and are listed in Table 1.

Phylogenetic analyses

The dataset of concatenated ITS1-5.8S-ITS2-nLSU sequences of the *Favolaschia* was analysed. Sequences of *Mycena seminau* A.L.C. Chew & Desjardin were used as outgroups (Chew et al. 2014). The newly-generated sequences in this study and additional sequences retrieved from Zhang et al. (2023) were partitioned to ITS1, 5.8S, ITS2, nrLSU and then aligned separately using MAFFT v.74 (http://mafft.cbrc.jp/alignment/server/, Katoh et al. 2017) with the G-INS-I iterative refinement algorithm and optimised manually in BioEdit v.7.0.5.3 (Hall 1999). The separate alignments were then concatenated using PhyloSuite v.1.2.2 (Zhang et al. 2020).

Maximum Likelihood (ML) analyses and Bayesian Inference (BI) were carried out by using RAxML v.8.2.10 (Stamatakis 2014) and MrBayes 3.2.6 (Ronquist and Huelsenbeck 2003), respectively. In ML analysis, statistical support values were obtained by using rapid bootstrapping with 1000 replicates, with default settings for other parameters. For BI, the best-fit partitioning scheme and substitution model were determined by using ModelFinder (Kalyaanamoorthy et al. 2017) via the “greedy” algorithm, branch lengths estimated as “linked” and AICc. Four Markov chain Monte Carlo chains (one cold) were constructed for 5,000,000 generations, with sampling every 1000 generations. Convergence was assessed as the standard deviation of split frequencies < 0.01. The first quarter of the trees, which represented the burn-in phase of the analyses, were discarded and the remaining trees were used to calculate posterior probabilities (BPP) in the majority rule consensus tree.

Phylogenetic trees were visualised by using FigTree version 1.4.4 (Rambaut 2018). Branches that received bootstrap supports for ML (≥ 75%) and BPP (≥ 0.95) were considered as significantly supported. The best topologies from ML analyses are shown in this study and the final alignments and the retrieved topologies were deposited in TreeBASE (http://treebase.org/treebase-web/home.html), under accession ID: 30973.

Results

Phylogenetic analyses

In this study, the combined ITS1-5.8S-ITS2-nLSU dataset included sequences from 113 specimens, representing 34 species of *Favolaschia* and one species of *Mycena* (Pers.) Roussel as the outgroup (Table 1, Fig. 2). ModelFinder suggested models were HKY+F+G4 for ITS1+ITS2, K2P+G4 for 5.8s and K2P+G4 for nLSU, for the Bayesian analysis. The BI analysis resulted in a concordant topology with an average standard deviation of split frequencies of 0.008584. The ML and BI analyses resulted in nearly identical topologies and only the ML

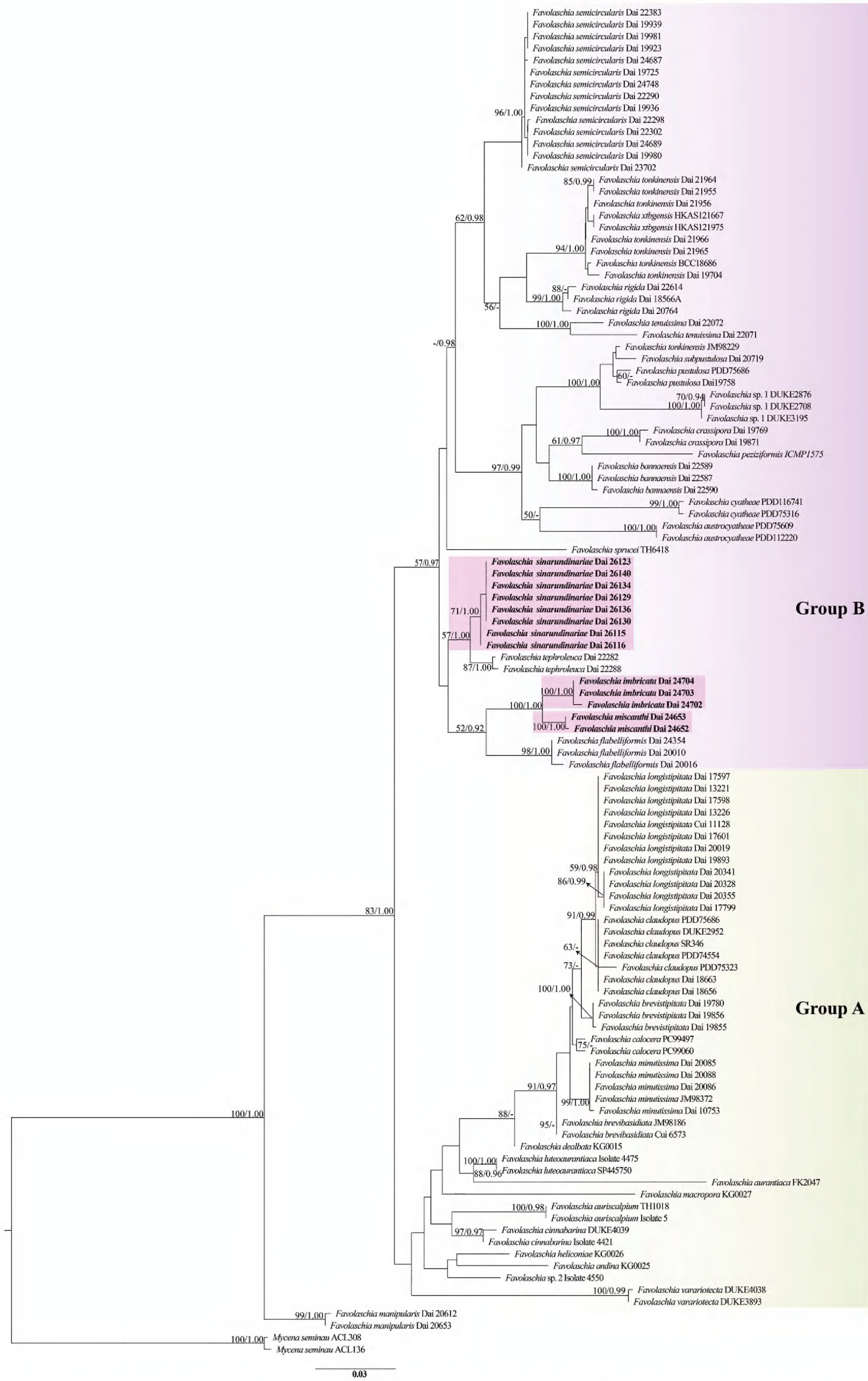

Figure 2. Maximum Likelihood (ML) tree illustrating the phylogeny of *Favolaschia*, based on a combined ITS1-5.8S-ITS2-nLSU-mtSSU-nuSSU dataset. Branches are labelled with parsimony bootstrap values (ML) higher than 50% and Bayesian Posterior Probabilities (BPPs) more than 0.90. (Group A: *Favolaschia* sect. *Favolaschia*; Group B: *Favolaschia* sect. *Anechinus*)

Table 1. Names, specimen numbers, locality and corresponding GenBank accession numbers of the taxa used in this study.

Species	Specimen no.	Locality	ITS no.	nLSU no.
Favolaschia andina	KG0025	Panama	HM246678	HM246679
F. aurantiaca	FK2047	Brazil	JX987670	–
F. aurantiaca	KG0013	Panama	–	HM246676
F. auriscalpium	Isolate 5	–	KY649461	–
F. auriscalpium	TH1018	Guyana	DQ026241	–
F. austrocyatheae	PDD75609	New Zealand	NR132809	–
F. austrocyatheae	PDD75609	New Zealand	DQ026257	–
F. bannaensis	Dai 22587	Yunnan, China	ON870497	ON870473
F. bannaensis	Dai 22589	Yunnan, China	ON870498	ON870474
F. bannaensis	Dai 22590	Yunnan, China	ON870499	ON870475
F. brevibasidiata	Cui 6573	Hainan, China	MZ661794	–
F. brevibasidiata	JM98186	Yunnan, China	DQ026239	–
F. brevistipitata	Dai 19780	Yunnan, China	MZ661772	MZ661742
F. brevistipitata	Dai 19855	Yunnan, China	MZ661773	MZ661743
F. brevistipitata	Dai 19856	Yunnan, China	MZ661774	MZ661744
F. calocera	PC99060	Madagascar	DQ26252	–
F. calocera	PC99497	Madagascar	DQ026253	–
F. cinnabarina	Isolate 4421	Brazil	JX987669	–
F. cinnabarina	RVPR82	–	–	AF261416
F. claudopus	Dai 18656	Australia	MZ661775	MZ661735
F. claudopus	Dai 18663	Australia	MZ661776	MZ661734
F. claudopus	SR346	Kenya	DQ026237	–
F. claudopus	PDD74554	New Zealand	DQ026251	–
F. claudopus	PDD75323	New Zealand	DQ026248	–
F. claudopus	PDD75686	New Zealand	DQ026249	–
F. claudopus	DUKE2952	New Zealand	DQ026238	–
F. crassipora	Dai 19769	Yunnan, China	ON870500	ON870476
F. crassipora	Dai 19871	Yunnan, China	ON870501	ON870477
F. cyatheae	PDD75316	New Zealand	NR132808	–
F. cyatheae	PDD75316	New Zealand	DQ026256	–
F. dealbata	KG0015	Panama	–	HM246677
F. flabelliformis	Dai 20010	Yunnan, China	ON870502	ON870478
F. flabelliformis	Dai 20016	Yunnan, China	ON870503	–
F. flabelliformis	Dai 24354	Yunnan, China	**OR271272**	**OR260441**
F. heliconiae	KG0026	Panama	–	HM246680
F. imbricata	**Dai 24702**	**Guangdong, China**	**OR334876**	–
F. imbricata	**Dai 24703**	**Guangdong, China**	**OR334877**	**OR334881**
F. imbricata	**Dai 24704**	**Guangdong, China**	**OR334878**	**OR334882**
F. longistipitata	Dai 13221	Yunnan, China	MZ661777	–
F. longistipitata	Dai 13226	Yunnan, China	MZ661778	–
F. longistipitata	Cui 11128	Yunnan, China	MZ661779	–
F. longistipitata	Dai 17597	Yunnan, China	MZ661780	–
F. longistipitata	Dai 17598	Yunnan, China	MZ661781	–

Species	Specimen no.	Locality	ITS no.	nLSU no.
F. longistipitata	Dai 17601	Yunnan, China	MZ661782	–
F. longistipitata	Dai 19799	Yunnan, China	MZ661784	MZ661739
F. longistipitata	Dai 19893	Yunnan, China	MZ661785	MZ661740
F. longistipitata	Dai 20019	Yunnan, China	MZ661786	MZ661741
F. longistipitata	Dai 20328	Yunnan, China	MZ661787	–
F. longistipitata	Dai 20341	Yunnan, China	MZ661788	–
F. longistipitata	Dai 20355	Yunnan, China	MZ661789	–
F. luteoaurantiaca	Isolate 4475	–	JX987667	–
F. luteoaurantiaca	SP445750	Brazil	NR132874	–
F. macropora	KG0027	Panama	NR132845	HM246682
F. manipularis	Dai 20612	Yunnan, China	MZ801776	MZ914395
F. manipularis	Dai 20653	Yunnan, China	MZ801777	–
F. minutissima	JM98372	Thailand	DQ026240	–
F. minutissima	Dai 10753	Hainan, China	MZ661790	–
F. minutissima	Dai 20085	Hainan, China	MZ661791	MZ661736
F. minutissima	Dai 20086	Hainan, China	MZ661792	MZ661737
F. minutissima	Dai 20088	Hainan, China	MZ661793	MZ661738
F. miscanthi	**Dai 24652**	**Guangxi, China**	**OR334879**	**OR334883**
F. miscanthi	**Dai 24653**	**Guangxi, China**	**OR334880**	**OR334884**
F. peziziformis	ICMP1575	Japan	DQ026255	–
F. peziziformis	PDD67440	New Zealand	–	AY572008
F. pustulosa	PDD75686	New Zealand	DQ026254	–
F. pustulosa	Dai 19758	Yunnan, China	MT292325	MT293226
F. rigida	Dai 18566A	Guangxi, China	ON870504	ON870479
F. rigida	Dai 20764	Yunnan, China	ON870505	ON870480
F. rigida	Dai 22614	Fujian, China	ON870506	–
F. semicircularis	Dai 19725	Guangdong, China	ON870507	ON870481
F. semicircularis	Dai 19923	Yunnan, China	ON870508	ON870482
F. semicircularis	Dai 19936	Yunnan, China	ON870509	ON870483
F. semicircularis	Dai 19939	Yunnan, China	ON870510	–
F. semicircularis	Dai 19980	Yunnan, China	ON870511	ON870484
F. semicircularis	Dai 19981	Yunnan, China	ON870512	ON870485
F. semicircularis	Dai 22290	Zhejiang, China	ON870513	ON870486
F. semicircularis	Dai 22298	Zhejiang, China	ON870515	ON870488
F. semicircularis	Dai 22302	Zhejiang, China	ON870516	–
F. semicircularis	Dai 23702	Hunan, China	**OR271273**	**OR260442**
F. semicircularis	Dai 24689	Guangxi, China	**OR271274**	**OR260443**
F. semicircularis	Dai 24748	Jiangxi, China	**OR271275**	**OR260444**
F. semicircularis	Dai 24687	Guangxi, China	**OR271276**	**OR260445**
F. semicircularis	Dai 22383	Fujian, China	ON870517	–
F. sinarundinariae	**Dai 26115**	**Sichuan, China**	**OR575908**	**OR575906**
F. sinarundinariae	**Dai 26116**	**Sichuan, China**	**OR575909**	**OR575907**
F. sinarundinariae	**Dai 26123**	**Sichuan, China**	**OR855969**	**OR855975**
F. sinarundinariae	**Dai 26129**	**Sichuan, China**	**OR855970**	–
F. sinarundinariae	**Dai 26130**	**Sichuan, China**	**OR855971**	–

Species	Specimen no.	Locality	ITS no.	nLSU no.
F. sinarundinariae	**Dai 26131**	**Sichuan, China**	**OR855972**	–
F. sinarundinariae	**Dai 26134**	**Sichuan, China**	**OR855973**	**OR855976**
F. sinarundinariae	**Dai 26140**	**Sichuan, China**	**OR855974**	**OR855975**
F. sp. 1	DUKE2708	Australia	DQ026234	–
F. sp. 1	DUKE2876	Australia	DQ026235	–
F. sp. 1	DUKE3195	Papua New Guinea	DQ026236	–
F. sp. 2	Isolate 4550	Panama	JX987668	–
F. sprucei	TH6418	Guyana	DQ026246	–
F. subpustulosa	Dai 20719	Yunnan, China	ON870518	ON870489
F. tenuissima	Dai 22072	Hainan, China	ON870520	ON870491
F. tenuissima	Dai 22071	Hainan, China	ON870519	ON870490
F. tephroleuca	Dai 22282	Yunnan, China	ON870521	ON870492
F. tephroleuca	Dai 22288	Chongqing, China	ON870522	ON870493
F. tonkinensis	Dai 21955	Hainan, China	ON870523	ON870494
F. tonkinensis	Dai 21956	Hainan, China	ON870524	ON870495
F. tonkinensis	Dai 21964	Hainan, China	ON870525	–
F. tonkinensis	Dai 21965	Hainan, China	ON870526	ON870496
F. tonkinensis	Dai 21966	Hainan, China	ON870527	–
F. tonkinensis	Dai 19704	Guangdong, China	**OR271277**	**OR260446**
F. tonkinensis	BCC 18686	–	MN093316	MN093317
F. tonkinensis	JM98229	Yunnan, China	DQ026247	–
F. varariotecta	DUKE3893	Puerto Rico	DQ026243	–
F. varariotecta	DUKE4038	Puerto Rico	DQ026244	–
F. xtbgensis	HKAS 121667	Yunnan, China	OL413048	OL413044
F. xtbgensis	HKAS 121975	Yunnan, China	OL413036	OL413035
Mycena seminau	ACL136	Malaysia	KF537250	KJ206952
Mycena seminau	ACL308	Malaysia	KF537252	KJ206964

Notes: New sequences are in bold; "–" represents missing data.

tree is presented with the bootstrap supports for ML and BPP not less than 50% and 0.90, respectively.

The phylogeny is similar to those of Johnston et al. (2006), Magnago et al. (2013) and Zhang et al. (2023). All *Favolaschia* samples are clustered within two groups (A and B), which correspond to the sections proposed by Singer (1974): *Favolaschia* sect. *Favolaschia* (group A) and *F.* sect. *Anechinus* (group B), except *F. manipularis*. In this study, three new lineages with high support (100/1.00, 100/1.00 and 71/1.00, respectively) nest in *F.* sect. *Anechinus* (group B). Amongst them, five specimens from Guangdong and Guangxi formed two lineages and clustered into a clade with strong support (100/1.00), namely *F. imbricata* and *F. miscanthi*. Eight specimens from Sichuan formed a support lineage, namely *F. sinarundinariae*, sister to *Favolaschia tephroleuca*. Furthermore, similarity searches with the ITS barcoding from the three new species were performed using BLAST (http://www.ncbi.nlm.nih.gov/BLAST/) from NCBI and showed less than 95% identity, respectively, in the genus *Favolaschia*, which demonstrated the obvious nucleotide differences of the three species with other species in the genus.

Taxonomy

***Favolaschia imbricata* Q.Y. Zhang, L.S. Bian, F. Wu & Y.C. Dai, sp. nov.**
MycoBank No: 851807
Figs 3A, 4

Type. CHINA, Guangdong Province, Guangzhou, Baiyun District, Maofengshan Forest Park, dead bamboo, 15 Apr 2023, Dai 24702 (BJFC042256, holotype).

Etymology. "*imbricata*" (Lat.): refers to the species having imbricate basidiomata.

Macrostructures. Basidiomata annual, gregarious, gelatinous when fresh and dry. Pilei 2–5 × 1.5–3 mm, conchoid, semicircular to subcircular; pileal surface pale grey to greyish-white (B1) when fresh, dark grey or mouse-grey (1D1–1F1) upon drying, convex with a reticulate pattern matching the pores below, faintly pruinose when dry; margin incurved, entire; context thin. Hymenophore paler than pileal surface, greyish-white (B1) when fresh and ash-grey (1B1–1C1) when dry, poroid, about 22–55 pores per basidiomata; mature pores 0.2–0.6 mm diam., polygonal, larger near the base and smaller near the edge, the marginal pores often incomplete; tubes up to 0.3 mm long. Stipe absent.

Microstructures. Basidiospores (6.8–)7–9 × 5–6.8 µm, L = 7.92 µm, W = 5.84 µm, Q = 1.31–1.38 (*n* = 90/3), broadly ellipsoid to subglobose, hyaline, thin-walled, smooth, with some guttules, faintly IKI+, CB–. Basidia 24–30 × 7–13 µm, cylindrical or clavate with some guttules, 4–spored, sterigmata 3–6 µm long; basidioles similar in shape to the basidia, but slightly smaller. Gloeocystidia and acanthocystidia absent. Cheilocystidia 25–39 × 7–14 µm, present at dissepiment edge, cylindrical or clavate, with obtuse diverticulate projections at the apex, thin-walled. Pileipellis hyphae subparallel, smooth to diverticulate, thin-walled, 5–11 µm diam.; terminal cells cystidioid or pyriform, smooth, thin-walled. Tramal hyphae subparallel, widely spaced in a gelatinous matrix, some with dense contents, some collapsed, thin-walled, 2–5 µm diam. Clamp connections present.

Additional specimens examined. CHINA, Guangdong Province, Guangzhou, Baiyun District, Maofengshan Forest Park, dead bamboo, 15 Apr 2023, Dai 24703 (BJFC042257, paratype), Dai 24704 (BJFC042258, paratype).

Distribution and ecology. *Favolaschia imbricata* is distributed in subtropical area of Guangdong Province, China; it grows on dead bamboo and causes a white rot.

***Favolaschia miscanthi* Q.Y. Zhang, L.S. Bian, F. Wu & Y.C. Dai, sp. nov.**
MycoBank No: 851808
Figs 3B, 5

Type. CHINA, Guangxi Autonomous Region, Hezhou, Dazhongshan Forest Park, rotten *Miscanthus*, 19 Apr 2023, Dai 24652 (BJFC042179, holotype).

Etymology. "*miscanthi*" (Lat.): refers to the species inhabiting rotten *Miscanthus*.

Macrostructures. Basidiomata annual, gregarious, gelatinous when fresh and dry. Pilei 3–6 × 1.5–4 mm, conchoid or semicircular; pileal surface satin white (1A1–2A1) when fresh and drying, convex, transparent with a reticulate pattern matching the pores below, glabrous; margin straight, crenulate; context

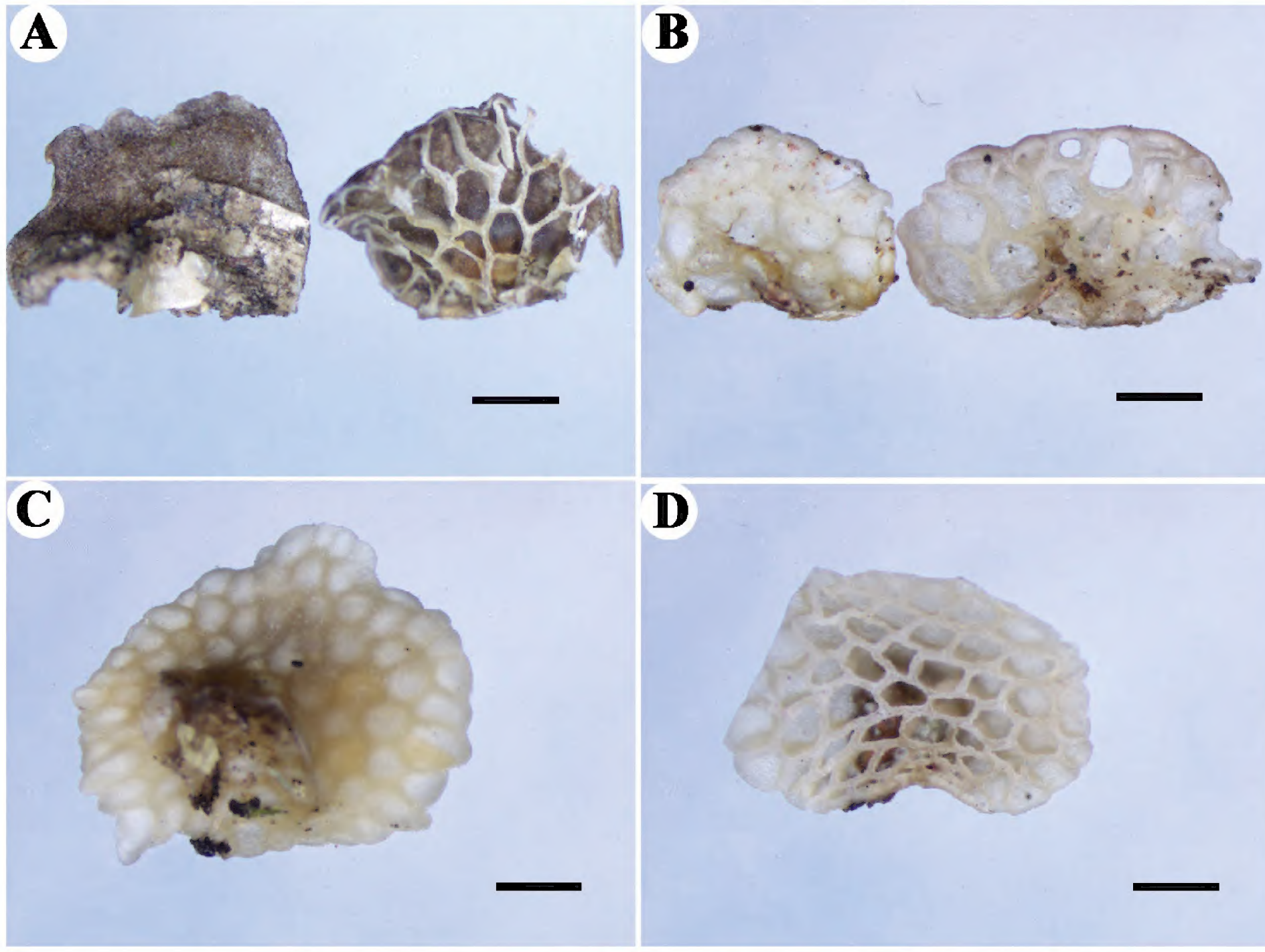

Figure 3. Dry basidiomata of *Favolaschia* species **A** *Favolaschia imbricata* **B** *Favolaschia miscanthi* **C, D** *Favolaschia sinarundinariae*. Scale bars: 1 mm.

thin, transparent. Hymenophore concolorous with pileal surface, poroid, up to 40 pores per basidiocarp; mature pores 0.5–1 mm diam., polygonal, larger near the base and smaller near the edge, the marginal pores often incomplete; tubes up to 0.4 mm long. Stipe absent.

Microstructures. Basidiospores 7.5–10 × 5.5–7(–7.5) µm, L = 8.90 µm, W = 6.28 µm, Q = 1.37–1.46 (*n* = 60/2), broadly ellipsoid to subglobose, hyaline, thin-walled, smooth, with some guttules, faintly IKI+, CB–. Basidia 32–45 × 7–10 µm, narrowly clavate, tapered towards the base, apex broadly rounded, 4–spored, sterigmata 2–8 µm long; basidioles similar in shape to the basidia, but slightly smaller. Gloeocystidia and acanthocystidia absent. Cheilocystidia 17–34 × 7–10 µm, present at dissepiment edge, broom-shaped or irregular with small diverticulate projections on the sides and at the apex, thin-walled. Pileipellis hyphae interwoven, smooth to diverticulate, thin-walled, 4–7 µm in diam.; terminal cells cylindrical or clavate, with obtuse diverticulate projections at the apex, orientated perpendicular to pileal surface. Tramal hyphae interwoven, widely spaced in a gelatinous matrix, some with dense contents, some collapsed, thin-walled, 2–6 µm in diam. Clamp connections present.

Additional specimen examined. China, Guangxi Autonomous Region, Hezhou, Dazhongshan Forest Park, rotten *Miscanthus*, 19 Apr 2023, Dai 24653 (BJFC042180, paratype).

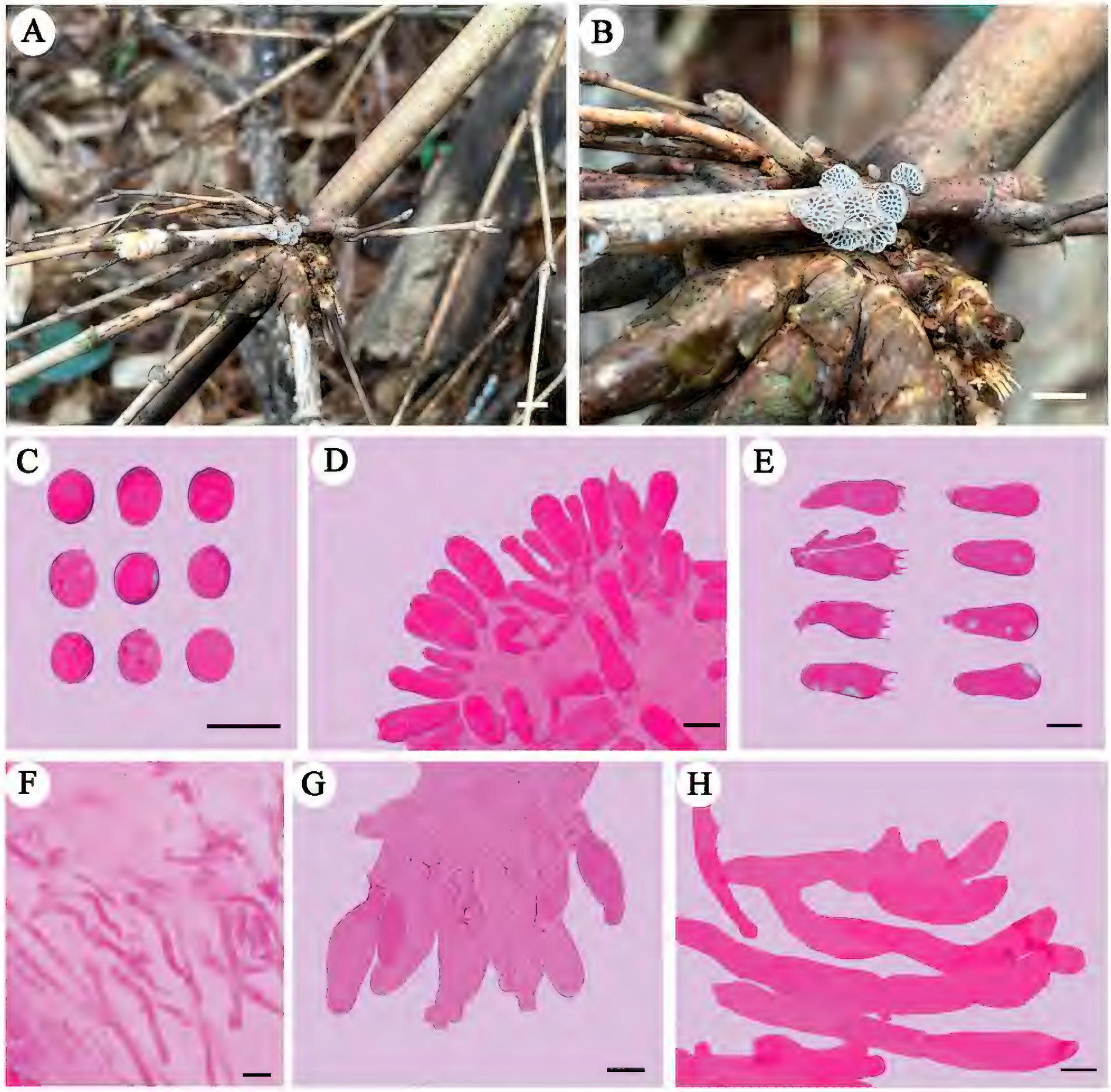

Figure 4. Basidiomata and microscopic structures of *Favolaschia imbricata* **A, B** basidiomata (Dai 24702, holotype) **C** basidiospores **D** hymenium in trama **E** basidia and basidioles **F** tramal hyphae **G** cheilocystidia at dissepiment edge **H** hyphae of pileipellis. Scale bars: 5 mm (**A, B**); 10 μm (**C–H**).

Distribution and ecology. *Favolaschia miscanthi* is distributed in the subtropical area of the Guangxi Autonomous Region, China; it grows on rotten *Miscanthus* and causes white rot.

***Favolaschia sinarundinariae* Q.Y. Zhang, L.S. Bian, F. Wu & Y.C. Dai, sp. nov.**
MycoBank No: 851809
Figs 3C, D, 6

Type. China, Sichuan Province, Bazhong, Nanjiang County, Micangshan National Forest Park, 25 Sep 2023, dead *Sinarundinaria*, Dai 26123 (BJFC043673, holotype).

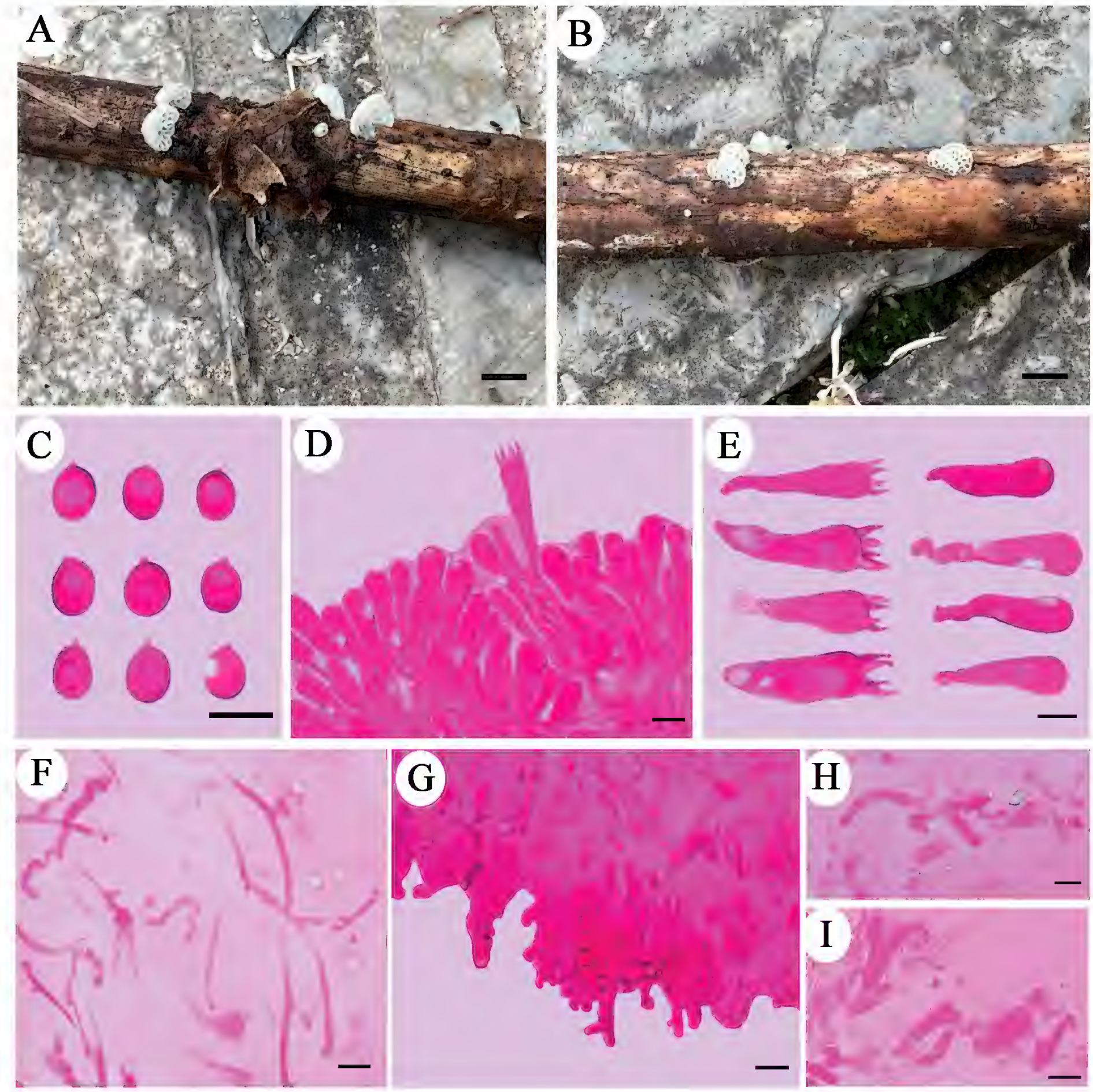

Figure 5. Basidiomata and microscopic structures of *Favolaschia miscanthi* **A, B** basidiomata (**A** Dai 24652, holotype **B** Dai 24653) **C** basidiospores **D** hymenium in trama **E** basidia and basidioles **F** tramal hyphae **G** cheilocystidia at dissepiment edge **H** hyphae of pileipellis **I** terminal cells of pileipellis. Scale bars: 5 mm (**A, B**); 10 μm (**C–I**).

Etymology. "*sinarundinariae*" (Lat.): refers to the species inhabiting dead *Sinarundinaria*.

Macrostructures. Basidiomata annual, gregarious, gelatinous when fresh and dry. Pilei 4–7 × 2–5 mm, conchoid to elliptic; pileal surface greyish-white (1B1) when fresh, dark grey (1F1) near the base upon drying, convex, transparent with a reticulate pattern matching the pores below, faintly pruinose when dry; margin straight, crenulate; context thin, opaque. Hymenophore concolorous with pileal surface, poroid, up to 80 pores per basidiomata; mature pores 0.4–1 mm diam., polygonal, the size varies irregularly, with some larger near the base or larger near the edges, the marginal pores often incomplete; tubes up to 0.5 mm long. Stipe absent.

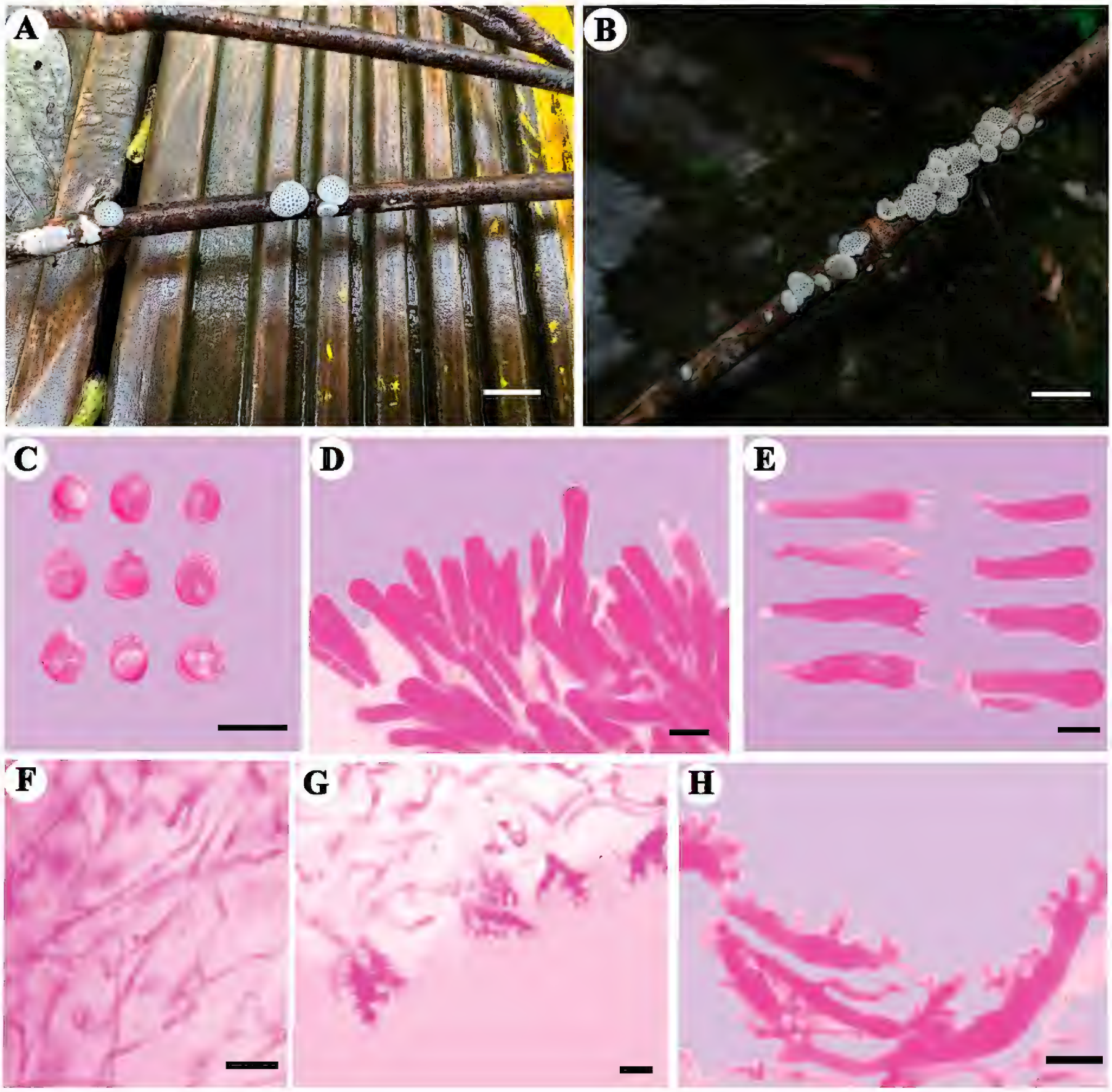

Figure 6. Basidiomata and microscopic structures of *Favolaschia sinarundinariae* **A, B** basidiomata (**A** Dai 26123, holotype **B** Dai 26116) **C** basidiospores **D** hymenium in trama **E** basidia and basidioles **F** tramal hyphae **G** cheilocystidia at dissepiment edge **H** hyphae and terminal cells of pileipellis. Scale bars: 1 cm (**A, B**); 10 μm (**C–H**).

Microstructures. Basidiospores 7–9 × 5–7(–7.5) μm, L = 7.87 μm, W = 6.08 μm, Q = 1.27–1.31 (*n* = 60/2), broadly ellipsoid to subglobose, hyaline, thin-walled, smooth, with some guttules, faintly IKI+, CB–. Basidia 40–50 × 7–9 μm, narrowly clavate, tapered towards the base, apex broadly rounded, 2 or 4–spored, sterigmata 5–10 μm long; basidioles similar in shape to the basidia, but slightly smaller. Gloeocystidia and acanthocystidia absent. Cheilocystidia 15–32 × 7–10 μm, present at dissepiment edge, antler-shaped or irregular with small diverticulate projections on the sides and at the apex, thin-walled. Pileipellis hyphae interwoven, with frequent diverticulate, thin-walled, 2–4 μm in diam., swollen to 8 μm on terminal; terminal cells irregular, with obtuse diverticulate projections at the apex, orientated perpendicular to pileal surface. Tramal hyphae interwoven, widely spaced in a gelatinous matrix, some with dense contents, some collapsed, thin-walled, 1.5–3 μm in diam. Clamp connections present.

Additional specimens examined. CHINA, Sichuan Province, Bazhong, Nanjiang County, Micangshan National Forest Park, 25 Sep 2023, dead *Sinarundinaria*, Dai 26129 (BJFC043679, paratype), Dai 26130 (BJFC, paratype), Dai 26134 (BJFC, paratype), Dai 26136 (BJFC, paratype), Dai 26142 (BJFC043692, paratype); Leshan, Ebian County, Heizhugou, 11 Aug 2023, dead *Sinarundinaria*, Dai 26115 (BJFC043665, paratype), Dai 26116 (BJFC043666, paratype).

Distribution and ecology. *Favolaschia sinarundinariae* is distributed in the subtropical area of Sichuan Province, China; it grows on rotten *Sinarundinaria* and causes white rot.

Discussion

The earliest records of *Favolaschia* species in China date back to the 20th century (Liu 1994; Liu and Yang 1994). Recently, with the application of molecular systematics, the species of *Favolaschia* in China have been continually updated (Liu 2020; Tolgor et al. 2021; Zhang and Dai 2021; Zhang et al. 2023). Morphological examination and phylogenetic analyses identified 16 species of *Favolaschia* in China (Zhang and Dai 2021; Zhang et al. 2023). In this study, three new species of *Favolaschia* are identified in south China: *Favolaschia imbricata*, *F. miscanthi* and *F. sinarundinariae*.

Phylogenetic studies of *Favolaschia* largely support the section classification, based on morphology proposed by Singer (1974). Morphologically, the *F.* sect. *Anechinus* includes two subsections, *F.* subsect. *Rubrinae* and *F.* subsect. *Depauperatae*, the former lacks gloeocystidia and gloeoporous hyphae (with granular contents); the latter has these structures, while the two subsections are not well distinguished in the phylogenetic tree. The three new species, *Favolaschia imbricata*, *F. miscanthi* and *F. sinarundinariae*, clustered within section *Anechinus* (group B), which is characterised by the lack of acanthocysts, gloeocystidia and gloeoporous hyphae replaced by irregular cystidia at the dissepiment edge or pileipellis.

In a combined ITS1-5.8S-ITS2-nLSU dataset-based phylogeny (Fig. 2), *Favolaschia imbricata* grouped with another new species *F. miscanthi*, with strong support (100/1.00). However, *Favolaschia miscanthi* can be easily distinguished from *F. imbricata* by its larger pores (0.5–1 mm vs. 0.2–0.6 mm), white pileal surface upon drying and growing on rotten *Miscanthus*, while *F. imbricata* shares dark grey or mouse-grey pileal surface upon drying and grows on dead bamboo. Based on the sub-generic classification of *Favolaschia* by Singer (1974), *F. imbricata* belongs to *Favolaschia* sect. *Anechinus* subsect. *Rubrinae*, because it lacks acanthocystidia, gloeocystidia and gloeoplerous hyphae.

Morphologically, *Favolaschia imbricata* with *F. flabelliformis* and *F. tonkinensis* share grey to greyish-white basidiomata when fresh and occur in south China. However, *F. flabelliformis* differs from *F. imbricata* by its flabelliform pilei and smaller pores (0.2–0.25 mm vs. 0.2–0.6 mm, Zhang et al. (2023)). *F. tonkinensis* differs from *F. imbricata* by its larger basidiomata (6–24 mm vs. 2–5 mm) and larger basidiospores (8–12.5 × 7–10.5 µm vs. 7–9 × 5–6.8 µm, Singer (1974)). In addition, *F. imbricata* has numerous cheilocystidia (cylindrical or clavate, with obtuse diverticulate projections at the apex) at the dissepiment edge, while they are absent in *F. flabelliformis* and *F. tonkinensis*.

Morphologically, *Favolaschia miscanthi* is characterised by its white basidiomata, inhabiting rotten *Miscanthus*, large pores (0.5–1 mm in diam.), broom-

shaped cheilocystidia and broadly ellipsoid to subglobose basidiospores (7.5–10 × 5.5–7 µm) and belongs to *F.* sect. *Anechinus* subsect. *Rubrinae*. Four species in *F.* subsect. *Rubrinae*, viz. *F. bannaensis*, *F. rigida*, *F. semicircularis* and *F. tenuissima*, resemble *F. miscanthi* by sharing smaller (< 2 cm) and pure white to white basidiomata when fresh and occur in south China. However, *Favolaschia bannaensis* differs from *F. miscanthi* by its larger pores (up to 1.5 mm vs. up to 1 mm) and inhabit bamboo or rotten angiosperms (Zhang et al. 2023). *Favolaschia rigida* differs from *F. miscanthi* by its obvious stipe, smaller pores (0.25–0.33 mm vs. up to 0.5–1 mm) and the absence of cheilocystidia (Zhang et al. 2023). *Favolaschia semicircularis* is readily distinguished from *F. miscanthi* by its obvious stipe and shorter basidia (24–32 µm vs. 32–45 µm in length, Zhang et al. (2023)). *Favolaschia tenuissima* differs from *F. miscanthi* by its fewer pores (up to 20 vs. up to 40) and the presence of obvious stipe (Zhang et al. 2023).

Eight specimens from Heizhugou and Micangshan National Forest Park in Sichuan Province formed a support lineage (71/1.00) and there are two base pairs differences between them in the ITS regions and no differences in morphology. We described these as a new species, namely *Favolaschia sinarundinariae*. Phylogenetically, *Favolaschia sinarundinariae* and *F. tephroleuca* cluster together in a supported clade (57/1.00) within *Favolaschia* sect. *Anechinus*, with each forming highly-supported branches. However, *F. tephroleuca* is readily distinguished from *F. sinarundinariae* by its grey to dark grey pileal surface, when fresh and fewer pores (up to 40 vs. up to 80). Morphologically, *Favolaschia flabelliformis* is similar to *F. sinarundinariae* by sharing a similar pileal surface, the absence of stipe and almost the same size basidiospores (Zhang et al. 2023), but the former species has smaller basidiomata (2–3 mm vs. 4–7 mm), smaller pores (0.2–0.25 mm vs. 0.5–1 mm) and fewer pores (10–40 vs. up to 80, Zhang et al. (2023)). In addition, *F. flabelliformis* and *F. sinarundinariae* are phylogenetically distantly related.

During the investigations of *Favolaschia*, the information on distribution areas is obtained (Fig. 1). Regarding geographical distribution, *Favolaschia* is distributed in south China (the south Qinling-Huai River Line). In addition, an updated key to 19 species of *Favolaschia* is provided in the following.

A key to 19 species of *Favolaschia* found in China

1	Acanthocystidia present	**2**
–	Acanthocystidia absent	**5**
2	Basidiomata apricot orange when fresh	**3**
–	Basidiomata lemon chrome when fresh	**4**
3	Pilei < 5 mm	***F. minutissima***
–	Pilei > 5 mm	***F. brevibasidiata***
4	Stipe < 5 mm in length	***F. brevistipitata***
–	Stipe > 5 mm in length	***F. longistipitata***
5	Basidiomata campanulate	***F. manipularis***
–	Basidiomata conchoid, flabellate, reniform, semicircular or subcircular	**6**
6	Mature pilei > 2 cm in length	**7**
–	Mature pilei < 2 cm in length	**9**
7	Stipe present	***F. tonkinensis***
–	Stipe absent	**8**

8 Mature pores polygonal, 3–6 mm in width ..... ***F. pustulosa***
– Mature pores round, 1–2.3 mm in width ..... ***F. subpustulosa***
9 Gloeocystidia present **10**
– Gloeocystidia absent **11**
10 Basidiospores 4.5–5.5 µm in width ..... ***F. peziziformis***
– Basidiospores 7–10 µm in width ..... ***F. crassipora***
11 Pilei transparent **12**
– Pilei opaque **14**
12 Stipe present, 1–3 × 0.5–1 mm ..... ***F. tenuissima***
– Stipe absent **13**
13 Basidiomata inhabiting rotten *Miscanthus* ..... ***F. miscanthi***
– Basidiomata inhabiting dead bamboo (Bambusoideae) ..... ***F. bannaensis***
14 Pilei ash grey to fuscous or dark when fresh ..... ***F. tephroleuca***
– Pilei usually white to pale white when fresh **15**
15 Cheilocystidia present at dissepiment edge **16**
– Cheilocystidia absent **17**
16 Stipe usually present ..... ***F. semicircularis***
– Stipe absent **17**
17 Mature pores 0.2–0.6 mm in width ..... ***F. imbricata***
– Mature pores up to 1 mm in width ..... ***F. sinarundinariae***
18 Stipe present, with diverticulate hyphae in pileipellis ..... ***F. rigida***
– Stipe absent, without diverticulate hyphae in pileipellis ..... ***F. flabelliformis***

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Qiu-Yue Zhang and Wan-Ying Li designed the research and contributed to data analysis and interpretation. Qiu-Yue Zhang, Xin Zhang, Yu-Cheng Dai and Hong-Gao Liu prepared the samples and drafted the manuscript. Yu-Cheng Dai, Lu-Sen Bian and Fang Wu discussed the results and edited the manuscript. All authors contributed to the article and approved the submitted version.

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Data availability

The sequences are deposited in the GenBank database (Table 1).

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Supplementary material 1

Three new species of *Favolaschia* (Mycenaceae, Agaricales) from South China

Authors: Qiu-Yue Zhang, Hong-Gao Liu, Wan-Ying Li, Xin Zhang, Yu-Cheng Dai, Fang Wu, Lu-Sen Bian

Data type: nex

Explanation note: In this study, the final alignments and the retrieved topologies were deposited in TreeBASE (http://treebase.org/treebase-web/home.html), under accession ID: 30973. At the same time, we upload it as an attachment to the editor.

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